REMARKS/ARGUMENTS

In response to the final Office Action dated April 4, 2005, Applicants have amended the claims, which when considered with the following remarks, is deemed to place the present claims in condition for allowance, or at least in better condition for appeal.

In the first instance, Applicants through the undersigned, thank Examiner Baum for his time in conducing a telephone interview of this case on May 19, 2005. As indicated on the Interview Summary, no agreement was reached with respect to the pending claims. The substance of the interview is incorporated into Applicants' remarks set forth hereinbelow.

Claim 1 has been rejected under 35 U.S.C. § 112, first paragraph, as allegedly failing to comply with the written description requirement. In response to the rejection, Applicants have canceled claim 1 from the application without prejudice. Applicants reserve the right to prosecute the same or similar claims in a continuation application. Since claim 1 has been canceled from the application, the rejection of claim 1 under 35 U.S.C.§ 112, first paragraph is moot.

Claims 1-4, 7-17, 25, 28-44, 46-47, 49-50, 52-53, 79-81, 86-87, 90-92, 95-101 and 103-121 remain rejected and claim 138 is newly rejected under 35 U.S.C. § 112, first paragraph, as allegedly violative of the written description requirement. On page 5 of the Office action the Examiner has stated:

The Office contends that for claims drawn to SEQ ID NO:26 and SEQ ID NO:31, Applicants have fulfilled the written description requirement. The office contends that the disclosure on pages 18-23 and 36-51 of the specification does not provide written description support for claims drawn to degenerated nucleic acid molecules, nucleic acid molecule which are divergent, or which are divergent due to differences between alleles, or functional fragments, or nucleic acid molecules that hybridize under medium stringency, or nucleic acid molecules encoding a protein exhibiting 70% similarity to SEQ ID NO:4, or nucleic acid molecules encoding an immunologically active fragment of a cytokinin oxidase, or functional fragment of a cytokinin oxidase. The disclosure on pages 18-23 and 36-51 does not provide additional sequences that have been exemplified but rather the disclosure recites claim limitations and definitions.

The Examiner has also asserted that contrary to what Applicants asserted in the previously filed amendment, the information presented in Figure 2 *was* considered and that "Applicants' Figure 2 discloses four protein sequences, three from Arabidopsis and one from maize. According to the Examiner, Applicants have not presented a representative number of sequences from a representative number of plants. It is the Examiner's opinion that absent the additional information, undue trial and error experimentation would be required by one skilled in the art to determine which amino acids can be altered and which amino acids are required."

During the interview, Applicants through the undersigned, brought to the Examiner's attention that Figure 2 contains information about a dicot (*Arabidopsis*) and a monocot (maize). With respect to "a nucleic acid molecule encoding a protein with an amino acid sequence comprising the polypeptide as given in SEQ ID NO:32 and which is at least 70% similar to the amino acid sequence as given in SEQ ID NO:4", we directed the Examiner to Example 2 of the specification and discussed the fact that even within one species, e.g., *Arabidopsis*, four different CKX proteins exhibit very low amino acid

sequence identity. *See* Example 2A of the specification, where the sequence identity between AtCKX1 and AtCKX2 is as low as 38.2%, yet both proteins still function as cytokin oxidases and confer similar phenotype in the root. *See also* examples 3, 4, and 11 of the specification. Moreover, the fact that both sequences are from *Arabidopsis* does not in any way mean the written description requirement is not met since both proteins are functional not only in Arabidopsis but also in tobacco and rice. Applicants can submit data which supports this statement if requested by the Examiner.

In addition, Applicants have deleted elements (f), (g), and (h) of claims 2 and 3. The recitation of "or for altering root geotropism" has also been deleted from the preamble of claim 2. In view of the amendments to the claims and the foregoing remarks, withdrawal of the rejection of claims 1-4, 7-17, 25, 28-44, 46-47, 49-50, 52-53, 79-81, 86-87, 90-92, 95-101,103-121 and 138 under 35 U.S.C. § 112, first paragraph is warranted.

Claims 1-4, 7-17, 25, 28-44, 46-47, 49-50, 52-53, 79-81, 86-87, 90-92, 95-101 and 103-121 remain rejected and claim 138 is rejected under 35 U.S.C.§ 112, first paragraph, as allegedly directed to non-enabled subject matter. Applicants respectfully submit that many of the amendments to the claims discussed above should obviate the rejection under the enablement provision of 35 U.S.C. § 112, first paragraph. With respect to other objections, we direct the Examiner to page 34-35 of the amendment filed August 30, 2004 where, during the interview, the Examiner indicated that arguments set forth therein would be reconsidered. Specifically, Applicants repeat and reassert the following discussion which demonstrates ample enablement for practicing the presently claimed invention. For example, the specification teaches that using the standard assay

for cytokin oxidase activity (Motyka et al, 1996), it was demonstrated that transgenic plant lines expressing the different *Arabidopsis* AtCKX proteins indicate that AtCKX1, AtCKX2, AtCKX3, and AtCKX4 all encode proteins having cytokin oxidase activity. *See* specifcation, page 93, lines 22-28, and Table 6 (*AtCKXI transgenic*); page 100, line 30, to page 101, line 3 and Table 7 (*AtCKX2 transgenic*); page 108, lines 20-24 and Table 8 (*AtCKX3* transgenic); page 110, lines 10-14, and Table 9 (*AtCKX*4 transgenic). Thus, one skilled in the art could readily test a putative cytokinin oxidase protein for cytokinin oxidase activity using a standard assay. Such testing would not reasonably be considered undue experimentation by a skilled artisan.

Moreover, the specification teaches in a number of different places that the phenotypes observed for the different AtCKX transgenics are very similar. *See e.g.*, page 107, lines 18-24:

> The phenotypes observed for *AtCKX2* transgenics were very similar but not identical to the *AtCKX1* transgenics, which were in turn very similar but not identical to the results obtained for the tobacco transgenics. This confirms the general nature of the consequences of a reduced cytokinin content in these two plant species and therefore, similar phenotypes can be expected in other plant species as well.

See also, specification, page 109, lines 4-9: "[t]he phenotypes generated by overexpression of the *ATCKX3* gene in tobacco and *Arabidopsis* were basically similar as those of AtCKX1 and AtCKX2 expressing plants, i.e., enhanced rooting and dwarfing" and page 111, lines 4-6: "[t]he phenotypes generated by overexpression of the AtCKX4 gene in tobacco and *Arabidopsis* were basically the same as those of AtCKX1 and AtCKX2 expressing plants, i.e., enhanced rooting, reduced apical dominance, dwarfing and yellowing of intercostals regions in older leaves of tobacco."

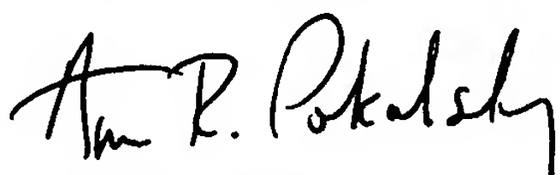
What becomes immediately apparent therefore, is that the specification clearly enables methods *inter alia*, for stimulating root growth, enhancing lateral root formation, and effecting the expression of cytokin oxidase polypeptides using nucleotide sequences encoding cytokinin oxidases having *as little as between 35% and 66% amino acid sequence similarity to each other!* If the specification enables these methods using such divergent cytokin oxidase proteins, surely the same methods are enabled using nucleic acids hybridizing under medium stringency hybridization conditions to a nucleotide sequence as set froth in SEQ ID NO:26, functional fragments of such nucleic acid molecules having cytokin oxidase activity, a nucleic acid molecule encoding an amino acid sequence comprising SEQ ID NO:32 and which is at least 70% similar to the amino acid sequence of SEQ ID NO:4, a nucleic acid molecule encoding an immunologically active fragment of a cytokinin oxidase encoded by SEQ ID NO:26 or any immunologically active fragment encoded by any of the nucleic acids specified in claim 3, a nucleic acid molecule encoding a functional fragment of a cytokinin oxidase encoded by SEQ ID NO:26 or any previously mentioned sequence. In view of the amendments to the claims and the foregoing remarks, withdrawal of the rejection of claims 1-4, 7-17, 25, 28-44, 46-47, 49-50, 52-53, 79-81, 86-87, 90-92, 95-101, 103-121 and 138 as allegedly non-enabled is respectfully requested.

Claims 1-4, 7-17, 25, 28-44, 49-50, 52-53, 87 and 98-101 remain rejected and claim 138 is newly rejected under 35 U.S.C. §102(b) as allegedly anticipated by Morris (February, 1999, WO 99/06571). In response to the rejection, claims 2 and 3 have been amended to recite in relevant part: "an isolated nucleic acid molecule specifically hybridizing to SEQ ID NO: 26, or to the complement thereof under medium stringency

conditions such as 1-4X SSC/0.25 % w/v SDS at 45° C or higher for 2 -3 hours, with the proviso that an isolated nucleic acid molecule encoding a cytokinin oxidase from corn (maize) is not included." As presently amended therefore, the rejected claims no longer encompass the cytokinin oxidase taught by Morris. Withdrawal of the rejection of claims 1-4, 7-17, 25, 28-44, 49-50, 52-53, 87, 98-101, and 138 under 35 U.S.C.§ 102(b) is therefore warranted.

In view of the foregoing remarks and amendments, it is respectfully submitted that the present case is in condition for allowance, which action is earnestly solicited.

Respectfully submitted



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